

Sequence Search Summary

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 08:37:17 ; Search time 6073 Seconds
(without alignments)
11283.324 Million cell updates/sec

Title: US-09-938-641-1
Perfect score: 1675
Sequence: 1 gccaacccgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%			Query			ID	Description
No.	Score	Match	Length	DB						
1	1675	100.0	1675	6	AX394436	Apple's WO			AX394436	Sequence
2	1675	100.0	337200	1	AP005280	Nakagawa Gen Bank			AP005280	Corynebac
3	1675	100.0	349980	6	AX127149	" EP1108790			AX127149	Sequence -Seg 7065
4	981	58.6	981	6	AX122198				AX122198	Sequence
5	981	58.6	981	6	BD164315				BD164315	Novel pol
6	781.2	46.6	303250	1	AP005220				AP005220	Corynebac
7	357	21.3	2550	6	AX122197				AX122197	Sequence
8	357	21.3	2550	6	BD164314				BD164314	Novel pol
9	235.8	14.1	1665	1	MAU18263				MAU18263	Mycobacteri
10	220.8	13.2	311000	1	SCO939122				SCO939122	Streptomy
11	217.2	13.0	3014	1	AF186371				AF186371	Streptomy
12	207.2	12.4	1901	1	AF034861				AF034861	Mycobacte
c 13	202	12.1	302300	1	AP005034				AP005034	Streptomy
14	195.8	11.7	1365	1	AF127219				AF127219	Streptomy
c 15	180.4	10.8	342300	1	MLEPRTN8				MLEPRTN8	Mycobacte
c 16	173.2	10.3	37114	1	MSGB38COS				MSGB38COS	L01095 M. leprae g
17	167.6	10.0	710	1	MXU43810				MXU43810	Mycobacteri
18	160	9.6	788	1	MMU43811				MMU43811	Mycobacteri
19	135.2	8.1	13075	1	AE004946				AE004946	Pseudomon.
c 20	131.6	7.9	11418	1	AE012182				AE012182	Xanthomon
21	129	7.7	142665	1	AE016794				AE016794	Pseudomon
c 22	126.4	7.5	203050	1	AL646071				AL646071	Ralstonia
c 23	122.8	7.3	3300	1	ECU74302				ECU74302	Erwinia car
c 24	121.6	7.3	11376	1	AE011722				AE011722	Xanthomon
25	121.4	7.2	4027	1	XCU94336				XCU94336	Xanthomonas
26	121.4	7.2	4044	1	AF315582				AF315582	Pseudomon
c 27	117.4	7.0	10951	1	AE006027				AE006027	Caulobact
c 28	116.4	6.9	313518	1	AE016856				AE016856	Pseudomon
29	113.2	6.8	4910	1	AY040244				AY040244	Burkholde
30	106.6	6.4	1900	6	A00047				A00047	E.coli mor
31	106	6.3	1179	1	ECOXYRGEN				ECOXYRGEN	X52666 E.coli oxyR
32	106	6.3	1264	1	ECOOXYR				ECOOXYR	J04553 E.coli oxyR
33	106	6.3	1471	1	ECOXYR				ECOXYR	X16531 Escherichia

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 08:12:07 ; Search time 470 Seconds
(without alignments)
9620.338 Million cell updates/sec

Title: US-09-938-641-1
Perfect score: 1675
Sequence: 1 gccaacccgagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		%							
Result	Query								
No.	Score	Match	Length	DB	ID	Description			

1	1675	100.0	1675	24	ABL56944	Appl's DE		Corynebacterium Ox	
2	1675	100.0	349980	22	AAH68530	Nakagawa EP110770		glutamicum codin	
3	981	58.6	981	22	AAH67079	C glutamicum codin			
4	981	58.6	981	25	ACA00583	C. glutamicum deri			
5	357	21.3	2550	22	AAH67078	C glutamicum codin			
6	357	21.3	2550	25	ACA00582	C. glutamicum deri			
c 7	177	10.6	177	25	ACA00584	C. glutamicum deri			
8	106	6.3	1900	10	AAN91492	Escherichia coli m			
c 9	87.4	5.2	19619	22	AAF28527	Genomic fragment #			
c 10	85	5.1	1089	22	AAH67080	C glutamicum codin			
c 11	85	5.1	1089	25	ACA00586	C. glutamicum deri			
c 12	72.4	4.3	9922	23	AAS59594	Propionibacterium			
c 13	72.2	4.3	2058	9	AAN80093	Sequence of BamHI/			
c 14	72.2	4.3	2058	16	AAQ97857	P. aeruginosa tfdA			
15	69	4.1	886	24	ABK74064	Bacillus lichenifo			
c 16	65.8	3.9	918	25	ABZ41010	N. gonorrhoeae nuc			
17	65.8	3.9	918	25	ABZ41541	N. gonorrhoeae nuc			
18	65.2	3.9	705	22	AAH67844	C glutamicum codin			
c 19	65.2	3.9	1050	24	ABL56492	Nucleotide sequenc			
c 20	65.2	3.9	349980	22	AAH68533	C glutamicum codin			
c 21	65	3.9	344	21	AAC74498	Human ORFX ORF53 p			
c 22	65	3.9	344	24	ABN22057	Human ORFX polynuc			
23	64.6	3.9	19231	21	AAA81470	N. meningitidis pa			
24	64.6	3.9	349980	21	AAF21544	Neisseria meningit			
25	64.6	3.9	349980	24	ABQ81842	Bifidobacterium lo			
26	64.6	3.9	1437668	21	AAA81490	N. meningitidis B			
27	64.4	3.8	837	22	AAF88334	S. spinosa DNA fra			
28	64.4	3.8	45624	22	AAF88315	S. spinosa DNA fra			
c 29	64.4	3.8	50000	22	AAF88312	S. spinosa DNA fra			
c 30	64.4	3.8	80161	20	AAZ21501	DNA fragment of Sa			
c 31	62.8	3.7	13020	24	ABQ78873	S. roseosporus dap			
32	60.2	3.6	909	22	AAH65641	C glutamicum codin			
33	60.2	3.6	1311	24	ABA95150	C. glutamicum lysR			
34	60.2	3.6	349980	22	AAH68525	C glutamicum codin			
35	60.2	3.6	349980	22	AAH68526	C glutamicum codin			
36	59.2	3.5	2703	23	AAS92835	DNA encoding novel			
37	58.8	3.5	3390	22	AAF26986	B. lactofermentum			
c 38	58.2	3.5	1830121	17	AAT42063	Haemophilus influe			
39	57.8	3.5	103599	23	ABX04971	S. cinnamonensis m			
40	57.6	3.4	1364	24	ABA91926	Corynebacterium gl			
c 41	57.6	3.4	309400	22	AAH68534	C glutamicum codin			
42	56.6	3.4	924	22	AAH68193	C glutamicum codin			
43	56.2	3.4	903	25	ACA01299	C. glutamicum deri			
44	55.6	3.3	879	22	AAH65474	C glutamicum codin			
45	55.6	3.3	879	25	ACA02151	C. glutamicum deri			

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 11:04:33 ; Search time 392 Seconds
(without alignments)
9361.817 Million cell updates/sec

Title: US-09-938-641-1
Perfect score: 1675
Sequence: 1 gccaacgcagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1487832 seqs, 1095472286 residues

Total number of hits satisfying chosen parameters: 2975664

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PGPubs

US 20020197605-A1

SUMMARIES

Result		%	Query					
No.	Score	Match	Length	DB	ID		Description	
1	1675	100.0	1675	9	US-09-938-641-1	instant	Sequence 1, Appli	
2	1675	100.0	3309400	10	US-09-738-626-1	Nakagawa	Sequence 1, Appli	
3	981	58.6	981	10	US-09-738-626-2114		Sequence 2114, Ap	
4	357	21.3	2550	10	US-09-738-626-2113		Sequence 2113, Ap	
5	202	12.1	1008	14	US-10-156-761-3218		Sequence 3218, Ap	
c 6	202	12.1	9025608	14	US-10-156-761-1		Sequence 1, Appli	
7	106.4	6.4	951	14	US-10-156-761-3347		Sequence 3347, Ap	
8	86.6	5.2	891	14	US-10-156-761-7285		Sequence 7285, Ap	
c 9	85	5.1	1089	10	US-09-738-626-2115		Sequence 2115, Ap	
10	81	4.8	936	14	US-10-156-761-4774		Sequence 4774, Ap	
11	69	4.1	886	10	US-09-974-300-1355		Sequence 1355, Ap	
12	65.2	3.9	705	10	US-09-738-626-2879		Sequence 2879, Ap	
c 13	65.2	3.9	3309400	10	US-09-738-626-1		Sequence 1, Appli	
14	65	3.9	987	14	US-10-156-761-2141		Sequence 2141, Ap	
15	62.8	3.7	912	14	US-10-156-761-1515		Sequence 1515, Ap	
16	62.8	3.7	9025608	14	US-10-156-761-1		Sequence 1, Appli	
17	60.2	3.6	888	14	US-10-156-761-7214		Sequence 7214, Ap	
18	60.2	3.6	909	10	US-09-738-626-676		Sequence 676, App	
19	58.8	3.5	3390	10	US-09-767-878-1		Sequence 1, Appli	
c 20	58.2	3.5	1830121	14	US-10-329-960-1		Sequence 1, Appli	
21	58	3.5	2658	14	US-10-156-761-1562		Sequence 1562, Ap	
22	57.6	3.4	1364	9	US-09-826-909-1		Sequence 1, Appli	
23	57.2	3.4	876	14	US-10-156-761-1152		Sequence 1152, Ap	
24	56.6	3.4	924	10	US-09-738-626-3228		Sequence 3228, Ap	
25	56.4	3.4	963	14	US-10-156-761-5097		Sequence 5097, Ap	
26	56	3.3	924	14	US-10-156-761-5287		Sequence 5287, Ap	
27	55.6	3.3	879	10	US-09-738-626-509		Sequence 509, App	
c 28	53.2	3.2	6133	14	US-10-114-170-15		Sequence 15, Appl	
29	52.4	3.1	465	10	US-09-974-300-5814		Sequence 5814, Ap	
30	52.2	3.1	602	10	US-09-974-300-5894		Sequence 5894, Ap	
31	51	3.0	912	14	US-10-156-761-761		Sequence 761, App	
32	50	3.0	909	14	US-10-156-761-1341		Sequence 1341, Ap	
33	49.8	3.0	894	14	US-10-156-761-4980		Sequence 4980, Ap	
34	49.2	2.9	903	14	US-10-156-761-1615		Sequence 1615, Ap	
35	48.8	2.9	948	14	US-10-156-761-4907		Sequence 4907, Ap	
c 36	48.6	2.9	33719	15	US-10-080-170-651		Sequence 651, App	
37	48.2	2.9	918	14	US-10-156-761-6700		Sequence 6700, Ap	
38	48	2.9	520	14	US-10-184-644-332		Sequence 332, App	
39	48	2.9	520	14	US-10-184-634-332		Sequence 332, App	
c 40	47.6	2.8	520	14	US-10-184-644-332		Sequence 332, App	
c 41	47.6	2.8	520	14	US-10-184-634-332		Sequence 332, App	
42	46.4	2.8	897	14	US-10-156-761-6980		Sequence 6980, Ap	
c 43	45.8	2.7	390	9	US-09-790-399-7		Sequence 7, Appli	
44	45.2	2.7	570	14	US-10-156-761-1030		Sequence 1030, Ap	
45	44.6	2.7	868	10	US-09-974-300-1338		Sequence 1338, Ap	

ALIGNMENTS

RESULT 1
US-09-938-641-1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 09:10:43 ; Search time 3283 Seconds
(without alignments)
12400.243 Million cell updates/sec

Title: US-09-938-641-1
Perfect score: 1675
Sequence: 1 gccaacccgagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues.

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB		ID	Description
No.	Score	Match	Length	DB	ID			
1	87.2	5.2	557	28	BH015055		BH015055	TDGBU22TH
2	84.8	5.1	989	29	CNS01L69		AL149234	Anopheles
3	82.8	4.9	581	10	BG456831		BG456831	NF098B09P
4	82.2	4.9	503	10	BE323006		BE323006	NF011C03P
5	80.6	4.8	863	29	CNS01JCX		AL146882	Anopheles
6	77.8	4.6	770	29	CNS01HMH		AL144618	Anopheles
7	74.8	4.5	793	29	CNS01QXX		AL156709	Anopheles
c 8	74	4.4	984	29	BZ702112		BZ702112	PUBMK94TD
9	70.2	4.2	890	29	BZ560396		BZ560396	pacs2-164
10	67.8	4.0	1513	29	BZ568940		BZ568940	pacs2-164
11	66	3.9	1280	29	BZ578104		BZ578104	msh2_5716
12	64.4	3.8	394	28	AZ049643		AZ049643	GSSBru013
13	63.6	3.8	1056	29	BZ558383		BZ558383	pacs1-60_
c 14	59.6	3.6	629	28	AQ991551		AQ991551	Rfc02534
15	58.6	3.5	829	29	BZ564143		BZ564143	pacs2-164
c 16	56.4	3.4	719	29	BZ562021		BZ562021	pacs2-164
17	54.8	3.3	734	28	AY080301		AY080301	AY080301
18	54.4	3.2	1201	13	BX381961		BX381961	BX381961
19	54.2	3.2	861	29	BZ572433		BZ572433	msh2_2632
c 20	53.8	3.2	780	29	BZ560257		BZ560257	pacs2-164
21	53.6	3.2	451	29	BZ422864		BZ422864	id59d05.b
c 22	53.6	3.2	550	29	BZ424306		BZ424306	id59d05.g
23	53.2	3.2	721	29	BZ562255		BZ562255	pacs2-164
24	53.2	3.2	817	29	BZ566287		BZ566287	pacs2-164
25	53.2	3.2	887	29	BZ577325		BZ577325	msh2_5355
26	53	3.2	590	28	AZ934607		AZ934607	BJ_Ba000
c 27	53	3.2	787	28	AZ934759		AZ934759	BJ_Ba000
c 28	52.4	3.1	648	9	AA606945		AA606945	vm93e11.r
29	52.4	3.1	674	14	CA403566		CA403566	EL01N0503
c 30	52.4	3.1	1175	29	BZ568637		BZ568637	pacs2-164
c 31	51.8	3.1	924	29	CC136342		CC136342	NDL.65B10
32	51	3.0	897	29	BZ572451		BZ572451	msh2_2640
c 33	49.6	3.0	872	29	BZ551630		BZ551630	pacs1-60_
34	49.4	2.9	688	28	B07706		B07706	318P1A04311
c 35	49.4	2.9	1161	29	BZ556936		BZ556936	pacs1-60_
36	49.2	2.9	920	29	BZ569987		BZ569987	msh2_1113
37	49	2.9	720	28	BH370673		BH370673	AG-ND-140
38	49	2.9	844	29	BZ574523		BZ574523	msh2_3710
39	48.8	2.9	473	14	CD212636		CD212636	HS1_6_C01
40	48.8	2.9	1344	29	BZ568929		BZ568929	pacs2-164
c 41	48.6	2.9	610	28	AZ935198		AZ935198	BJ_Ba000
c 42	48.6	2.9	617	12	BI643687		BI643687	EM1_19_B0
c 43	48.6	2.9	783	28	AZ935171		AZ935171	BJ_Ba000
44	48.2	2.9	836	14	CB853302		CB853302	UI-CF-FN0
45	47.8	2.9	278	28	AZ302981		AZ302981	GSSBru192

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 09:14:58 ; Search time 124 Seconds
(without alignments)
5962.232 Million cell updates/sec

Title: US-09-938-641-1
Perfect score: 1675
Sequence: 1 gccaacgcagggcatttac.....ttactggcagcacgatgac 1675

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
	1	180.4	10.8	37030	4	US-08-311-731A-25		Sequence 25, Appl	
	2	133.4	8.0	2094	4	US-09-252-991A-7438		Sequence 7438, Ap	
	3	133.4	8.0	3012	4	US-09-252-991A-7498		Sequence 7498, Ap	
	4	79.6	4.8	1602	4	US-09-252-991A-6382		Sequence 6382, Ap	
	5	79.4	4.7	921	4	US-09-252-991A-3438		Sequence 3438, Ap	
c	6	79.4	4.7	984	4	US-09-252-991A-3477		Sequence 3477, Ap	
	7	79.4	4.7	1263	4	US-09-252-991A-3462		Sequence 3462, Ap	
c	8	79	4.7	945	4	US-09-252-991A-6167		Sequence 6167, Ap	
	9	77.6	4.6	732	4	US-09-252-991A-6298		Sequence 6298, Ap	
c	10	72.6	4.3	1392	4	US-09-252-991A-3486		Sequence 3486, Ap	
c	11	72.2	4.3	2058	1	US-08-358-117-1		Sequence 1, Appli	

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 13:17:53 ; Search time 6074 Seconds
(without alignments)
11281.466 Million cell updates/sec

Title: US-09-938-641-1
Perfect score: 1675
Sequence: 1 gccaacgcgagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1675	100.0	1675	6	AX394436		AX394436	Sequence
	2	1675	100.0	337200	1	AP005280		AP005280	Corynebac
	3	1675	100.0	349980	6	AX127149		AX127149	Sequence
	4	981	58.6	981	6	AX122198		AX122198	Sequence
	5	981	58.6	981	6	BD164315		BD164315	Novel pol
	6	357	21.3	2550	6	AX122197		AX122197	Sequence
	7	357	21.3	2550	6	BD164314		BD164314	Novel pol
c	8	85	5.1	1089	6	AX122199		AX122199	Sequence
c	9	85	5.1	1089	6	BD164316		BD164316	Novel pol
c	10	23	1.4	268984	3	AE001274	Leishmania	AE001274	Leishmani
c	11	21	1.3	238557	2	AC133482		AC133482	Rattus no
	12	21	1.3	240091	2	AC137350		AC137350	Rattus no
c	13	21	1.3	263545	2	AC107182		AC107182	Rattus no
	14	21	1.3	303250	1	AP005220		AP005220	Corynebac
c	15	20	1.2	20	6	AX394439		AX394439	Sequence
c	16	20	1.2	183	6	AX121529		AX121529	Sequence
c	17	20	1.2	183	6	BD163646		BD163646	Novel pol
c	18	20	1.2	1285	10	BC046342		BC046342	Mus muscu
c	19	20	1.2	1294	10	BC024048		BC024048	Mus muscu
c	20	20	1.2	1387	10	MMU251200		AJ251200	Mus muscu
c	21	20	1.2	2434	10	MMU245737		AJ245737	Mus muscu
c	22	20	1.2	5568	4	SSIFNG		X53085	S.scrofa DN
	23	20	1.2	11982	1	AE008075		AE008075	Agrobacte
	24	20	1.2	12023	1	AE009110		AE009110	Agrobacte
	25	20	1.2	152888	9	AC091491		AC091491	Homo sapi
c	26	20	1.2	154342	2	AP005695		AP005695	Oryza sat
	27	20	1.2	158169	2	AC141751		AC141751	Apis mell
c	28	20	1.2	162183	2	AP005822		AP005822	Oryza sat
	29	20	1.2	162949	9	AC090943		AC090943	Homo sapi
	30	20	1.2	181034	2	AC135486		AC135486	Rattus no
	31	20	1.2	189054	2	AC135272		AC135272	Rattus no
	32	20	1.2	194985	10	AC002406		AC002406	Mouse chr
c	33	20	1.2	195636	2	AC139391		AC139391	Rattus no

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 11:59:28 ; Search time 470 Seconds
(without alignments)
9620.338 Million cell updates/sec

Title: US-09-938-641-1
Perfect score: 1675
Sequence: 1 gccaacgcgagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description	
	No.	Score	Query Match Length DB ID				
	1	1675	100.0	1675	24	ABL56944	Corynebacterium Ox
	2	1675	100.0	349980	22	AAH68530	C glutamicum codin
	3	981	58.6	981	22	AAH67079	C glutamicum codin
	4	981	58.6	981	25	ACA00583	C. glutamicum deri
	5	357	21.3	2550	22	AAH67078	C glutamicum codin
	6	357	21.3	2550	25	ACA00582	C. glutamicum deri
c	7	177	10.6	177	25	ACA00584	C. glutamicum deri
c	8	85	5.1	1089	22	AAH67080	C glutamicum codin
c	9	85	5.1	1089	25	ACA00586	C. glutamicum deri
c	10	20	1.2	20	24	ABL56946	Corynebacterium Ox
c	11	20	1.2	183	22	AAH66410	C glutamicum codin
	12	20	1.2	204	25	ACA01550	C. glutamicum deri
c	13	20	1.2	748	22	AAL24182	Human breast cance
	14	20	1.2	349980	22	AAH68528	C glutamicum codin
	15	19	1.1	402	24	ABZ08413	Human leukocyte de
	16	19	1.1	530	24	ABZ08416	Human leukocyte de
c	17	19	1.1	1263	22	AAH68278	C glutamicum codin
c	18	19	1.1	1386	22	AAF67922	Corynebacterium gl
	19	19	1.1	3926	19	AAV29577	Pythium oligandrum
c	20	19	1.1	3926	19	AAV29577	Pythium oligandrum
	21	19	1.1	3926	19	AAV29576	Pythium oligandrum
c	22	19	1.1	3926	19	AAV29576	Pythium oligandrum
	23	19	1.1	3933	19	AAV29578	Pythium oligandrum
c	24	19	1.1	3933	19	AAV29578	Pythium oligandrum
c	25	19	1.1	44820	24	AAS19703	Reference sequence
	26	19	1.1	148567	25	ABS55500	Gene encoding huma
	27	19	1.1	309400	22	AAH68534	C glutamicum codin
	28	18	1.1	30	24	ABL56945	Corynebacterium Ox
	29	18	1.1	201	25	ABX20985	Human GDP-mannose
c	30	18	1.1	289	24	ABS51630	Human cDNA encodin
c	31	18	1.1	360	22	AAI93049	Human polynucleoti
c	32	18	1.1	423	21	AAC57932	Arachidonic acid m
c	33	18	1.1	423	21	AAC57933	Arachidonic acid m
c	34	18	1.1	423	21	AAC57934	Arachidonic acid m
c	35	18	1.1	423	21	AAC57935	Arachidonic acid m
	36	18	1.1	491	24	ABL87838	Human ovarian canc
	37	18	1.1	578	21	AAF10311	Fusarium venenatum
	38	18	1.1	723	21	AAC48808	Arabidopsis thalia
	39	18	1.1	723	24	ABZ13849	Arabidopsis thalia
c	40	18	1.1	922	22	AAH34856	Human colon cancer
c	41	18	1.1	922	24	ABL90444	Human polynucleoti
	42	18	1.1	925	21	AAA02110	Human colon cancer
	43	18	1.1	1024	21	AAC37755	Arabidopsis thalia
	44	18	1.1	1026	21	AAC48812	Arabidopsis thalia
	45	18	1.1	1049	21	AAC36711	Arabidopsis thalia

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 15:20:29 ; Search time 390 Seconds
(without alignments)
9409.826 Million cell updates/sec

Title: US-09-938-641-1
Perfect score: 1675
Sequence: 1 gccaacgcagggcatttac.....ttactggcagcacgatgac 1675

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1487832 seqs, 1095472286 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2975664

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					ID	Description
	No.	Score	Query Match	Length	DB		
	1	1675	100.0	1675	9	US-09-938-641-1	Sequence 1, Appli
	2	1675	100.0	3309400	10	US-09-738-626-1	Sequence 1, Appli
	3	981	58.6	981	10	US-09-738-626-2114	Sequence 2114, Ap
	4	357	21.3	2550	10	US-09-738-626-2113	Sequence 2113, Ap
c	5	85	5.1	1089	10	US-09-738-626-2115	Sequence 2115, Ap
c	6	20	1.2	20	9	US-09-938-641-4	Sequence 4, Appli
c	7	20	1.2	183	10	US-09-738-626-1445	Sequence 1445, Ap
	8	19	1.1	628	13	US-10-027-632-290181	Sequence 290181,
	9	19	1.1	882	13	US-10-027-632-173402	Sequence 173402,
	10	19	1.1	882	13	US-10-027-632-173403	Sequence 173403,
c	11	19	1.1	1263	10	US-09-738-626-3313	Sequence 3313, Ap
	12	19	1.1	1848	14	US-10-156-761-3041	Sequence 3041, Ap
	13	19	1.1	2658	14	US-10-156-761-1562	Sequence 1562, Ap
	14	19	1.1	148567	10	US-09-801-876B-3	Sequence 3, Appli
	15	19	1.1	148567	14	US-10-254-869-3	Sequence 3, Appli
	16	19	1.1	9025608	14	US-10-156-761-1	Sequence 1, Appli
c	17	19	1.1	9025608	14	US-10-156-761-1	Sequence 1, Appli
	18	18	1.1	25	14	US-10-098-263B-74396	Sequence 74396, A
	19	18	1.1	30	9	US-09-938-641-3	Sequence 3, Appli
	20	18	1.1	201	10	US-09-878-574-3044	Sequence 3044, Ap
c	21	18	1.1	289	14	US-10-043-487-210	Sequence 210, App
c	22	18	1.1	445	11	US-09-918-995-31696	Sequence 31696, A
	23	18	1.1	491	10	US-09-867-701-10816	Sequence 10816, A
	24	18	1.1	598	13	US-10-027-632-193306	Sequence 193306,
	25	18	1.1	598	13	US-10-027-632-193307	Sequence 193307,
	26	18	1.1	598	13	US-10-027-632-193308	Sequence 193308,
	27	18	1.1	603	13	US-10-027-632-277321	Sequence 277321,
c	28	18	1.1	656	13	US-10-027-632-104782	Sequence 104782,
	29	18	1.1	715	13	US-10-027-632-11980	Sequence 11980, A
	30	18	1.1	723	10	US-09-938-842A-1654	Sequence 1654, Ap
	31	18	1.1	754	13	US-10-027-632-152169	Sequence 152169,
c	32	18	1.1	875	13	US-10-027-632-145072	Sequence 145072,
c	33	18	1.1	875	13	US-10-027-632-145073	Sequence 145073,
c	34	18	1.1	922	14	US-10-106-698-1948	Sequence 1948, Ap
c	35	18	1.1	2049	13	US-10-027-632-97200	Sequence 97200, A
c	36	18	1.1	2049	13	US-10-027-632-100266	Sequence 100266,
c	37	18	1.1	2049	13	US-10-027-632-100267	Sequence 100267,
	38	18	1.1	2344	13	US-10-044-090-745	Sequence 745, App
	39	18	1.1	3091	11	US-09-983-000A-1	Sequence 1, Appli
	40	18	1.1	3828	14	US-10-156-761-2959	Sequence 2959, Ap
c	41	18	1.1	4465	10	US-09-964-824A-267	Sequence 267, App
c	42	18	1.1	4465	11	US-09-984-842-1	Sequence 1, Appli
	43	18	1.1	7941	10	US-09-954-456-1812	Sequence 1812, Ap
	44	18	1.1	7941	11	US-09-983-000A-5	Sequence 5, Appli
	45	18	1.1	8058	11	US-09-983-000A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-938-641-1

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 13:19:53 ; Search time 3283 Seconds
(without alignments)
12400.243 Million cell updates/sec

Title: US-09-938-641-1
Perfect score: 1675
Sequence: 1 gccaacccgagggcatttac.....ttactggcagcacgatgatc 1675

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
			Match	Length	Score	Length			
c	1	21	1.3	621	13	BU547356			BU547356 GM880013A
c	2	20	1.2	65	9	AA106910			AA106910 ml85b05.r
c	3	20	1.2	134	10	BE234275			BE234275 141082 MA
c	4	20	1.2	171	10	BE234087			BE234087 140686 MA
	5	20	1.2	207	10	BF703787			BF703787 MI-P-E4-a
	6	20	1.2	229	10	BF703194			BF703194 MI-P-E4-a
	7	20	1.2	230	13	BQ598937			BQ598937 MI-P-E4-a
c	8	20	1.2	234	9	AW619198			AW619198 540 MARC
	9	20	1.2	235	13	BQ599092			BQ599092 MI-P-E4-a
	10	20	1.2	324	10	BF703696			BF703696 MI-P-E4-a
	11	20	1.2	329	13	BQ599184			BQ599184 MI-P-E4-a
c	12	20	1.2	334	13	BY118299			BY118299 BY118299
	13	20	1.2	337	10	BF712465			BF712465 MI-P-E4-a
	14	20	1.2	338	10	BF703795			BF703795 MI-P-E4-a
	15	20	1.2	339	10	BF703649			BF703649 MI-P-E4-a
c	16	20	1.2	340	13	BY074579			BY074579 BY074579
c	17	20	1.2	345	13	BY038194			BY038194 BY038194
c	18	20	1.2	346	10	BF321002			BF321002 uz58b12.y
	19	20	1.2	350	13	BQ598958			BQ598958 MI-P-E4-a
c	20	20	1.2	353	9	AA110753			AA110753 mm01e05.r
c	21	20	1.2	354	13	BY186446			BY186446 BY186446
c	22	20	1.2	356	13	BY043325			BY043325 BY043325
c	23	20	1.2	357	10	BB870151			BB870151 BB870151
	24	20	1.2	357	13	BQ598946			BQ598946 MI-P-E4-a
c	25	20	1.2	361	14	CB600576			CB600576 AGENCOURT
c	26	20	1.2	365	13	BY082798			BY082798 BY082798
c	27	20	1.2	366	13	BY046045			BY046045 BY046045
c	28	20	1.2	367	13	BY060917			BY060917 BY060917
	29	20	1.2	372	10	BF703685			BF703685 MI-P-E4-a
c	30	20	1.2	373	13	BY050330			BY050330 BY050330
	31	20	1.2	374	10	BF703655			BF703655 MI-P-E4-a
c	32	20	1.2	377	13	BY055356			BY055356 BY055356
	33	20	1.2	380	13	BQ599370			BQ599370 MI-P-E4-a
c	34	20	1.2	381	13	BY297534			BY297534 BY297534
c	35	20	1.2	382	13	BY039115			BY039115 BY039115
	36	20	1.2	383	13	BQ598982			BQ598982 MI-P-E4-a
	37	20	1.2	384	10	BF712107			BF712107 MI-P-E4-a
c	38	20	1.2	385	13	BY035249			BY035249 BY035249
	39	20	1.2	390	13	BQ599035			BQ599035 MI-P-E4-a
	40	20	1.2	393	9	AV834076			AV834076 AV834076
c	41	20	1.2	393	28	BH342756			BH342756 CH230-890
	42	20	1.2	398	13	BQ599018			BQ599018 MI-P-E4-a
c	43	20	1.2	398	14	CB707657			CB707657 AMGNNUC:N
c	44	20	1.2	401	12	BJ267400			BJ267400 BJ267400
	45	20	1.2	401	13	BY600926			BY600926 BY600926

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 13:24:18 ; Search time 124 Seconds
(without alignments)
5962.232 Million cell updates/sec

Title: US-09-938-641-1
Perfect score: 1675
Sequence: 1 gccaacccgcagggcatttac.....ttactggcagcagcatgatc 1675

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	19	1.1	3926	2	US-08-731-722-1	Sequence 1, Appli
c 2	19	1.1	3926	2	US-08-731-722-1	Sequence 1, Appli
3	19	1.1	3926	2	US-08-731-722-2	Sequence 2, Appli
c 4	19	1.1	3926	2	US-08-731-722-2	Sequence 2, Appli
5	19	1.1	3933	2	US-08-731-722-3	Sequence 3, Appli
c 6	19	1.1	3933	2	US-08-731-722-3	Sequence 3, Appli
7	19	1.1	148567	4	US-09-801-876B-3	Sequence 3, Appli
c 8	18	1.1	423	4	US-09-641-638-566	Sequence 566, App
c 9	18	1.1	423	4	US-09-641-638-567	Sequence 567, App
c 10	18	1.1	423	4	US-09-641-638-568	Sequence 568, App
c 11	18	1.1	423	4	US-09-641-638-569	Sequence 569, App